Stem Cell Reports, Volume 2 Supplemental Information

Exosomes as Critical Agents of Cardiac

Regeneration Triggered by Cell Therapy

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Supplemental Discussion

Differences in baseline ejection fraction between different mouse strains

We noted a noticeably high baseline ejection fraction for these animals. We surmise that this difference is due to the different background strain of mice used in the knockouts (C57BL6). In all other experiments in the manuscript, the strain of mice used is SCID-Beige. SCID-Beige mice lack mature B and T cells as well as Natural Killer (NK) cells. This fundamental difference in immune competence likely accounts for the contrast in the baseline measurement as they respond to injury differently. In most of the experiments in this manuscript we chose the SCID-Beige mouse since they are permissive to human cells (which are the source of the CDC and the exosomes). However an appropriate control for the 146a KO mouse was a wild type from the same background strain which the BL6 background. This has been previously documented. Strain has previously been shown to be a significant determinant of wound healing after myocardial infarction (van den Borne et al., 2009).

MiR-146a effect on immune infiltration

Attenuating the inflammatory immune response is not necessarily abrogating it altogether. Innate immune cells including macrophages have been shown to play pro regenerative roles. Furthermore unpublished data from our lab show that macrophage trafficking is not affected by CDC treatment, but macrophages treated with CDCs do switch from an M1 (proinflammatory) to an anti-inflammatory and pro-healing phenotype M2.

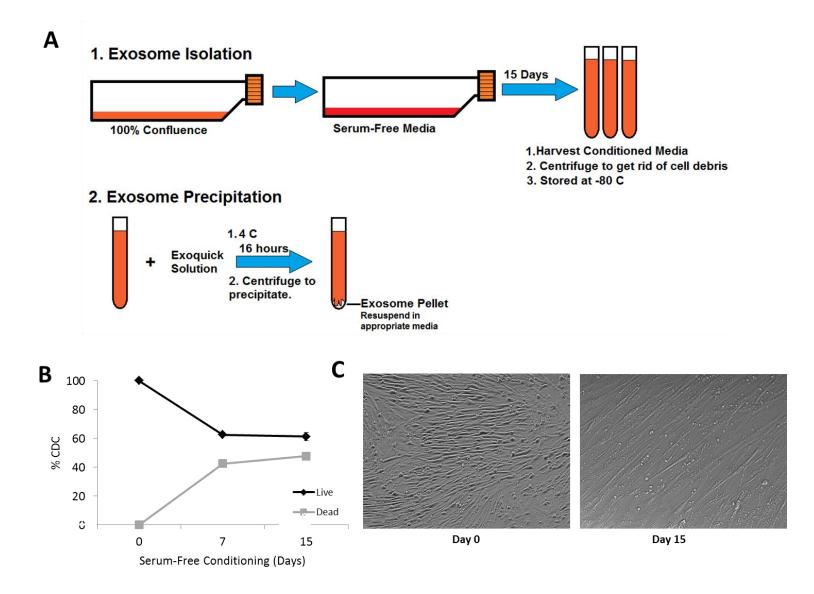
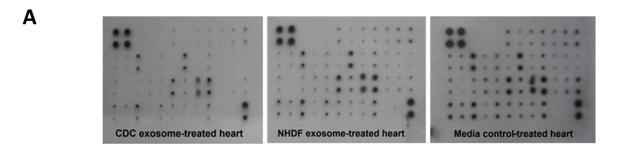


Figure S1. Isolation of exosomes from Cardiosphere-derived cells, Related to Figure 1

(A) Graphical representation of exosome isolation and purification for exosomes. (B) Cell viability (calcein) and cell death (Ethidium homodimer-1) assay performed on CDCs over the 15 day serum-free conditioning period. (C) Representative images of CDCs before and after serum-free conditioning.



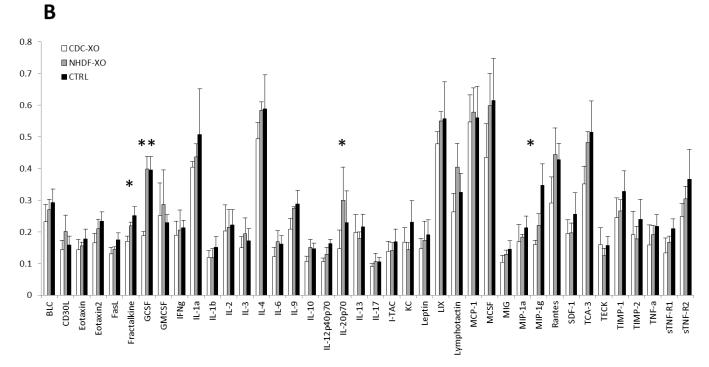


Figure S2. CDC exosomes reduce inflammation in a mouse model of acute MI, Related to Figure 2

(A) Representative protein arrays for 40 pro-inflammatory markers. (B) Quantification of inflammatory proteins in mouse hearts treated with CDC-exosomes, NHDF-exosomes, or control. Data comes from three mouse hearts per group. Analysis was done using one-way ANOVA (95% CI) (n=3 hearts per group). Data represented as mean and standard error of the mean.

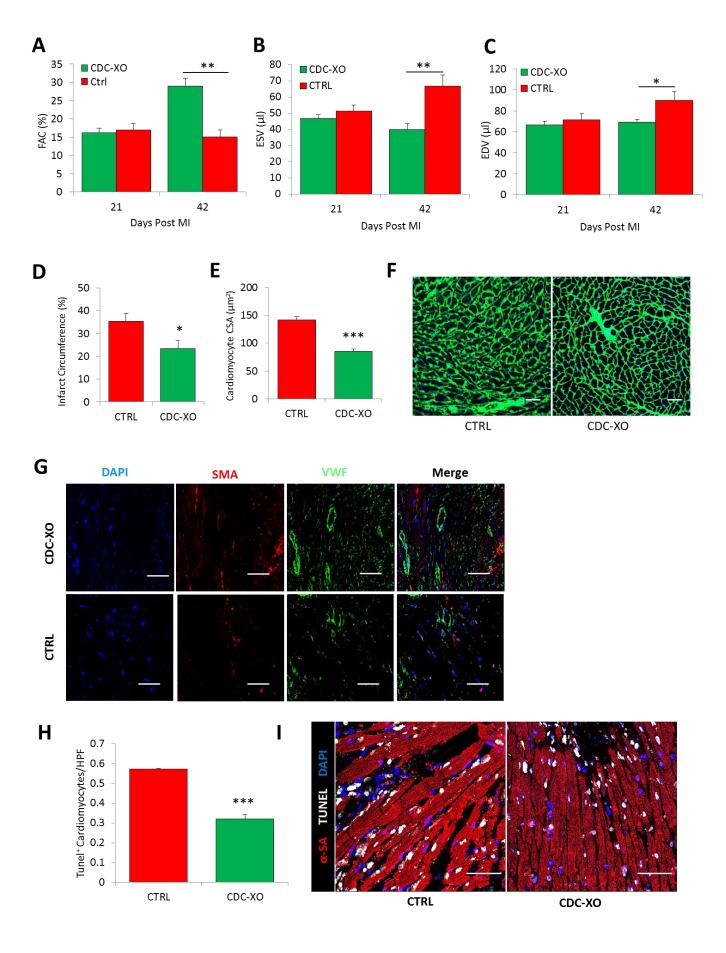


Figure S3. CDC-exosomes produce structural and functional benefits in mouse hearts after MI, Related to Figure 2

CDC-exosomes stimulate functional improvement and attenuate adverse remodeling and cardiac hypertrophy in a mouse model of chronic MI (a) Animals treated with CDC-exosomes showed significant functional improvement compared to control as shown by fractional area change (A) , end systolic volume (B) and end diastolic volume (C) (A-C, n=6 animals per group). Animals treated with CDC-exosomes also showed structural improvements as noted as seen in percent of the circumference of tissue sections that are scar (D), decreased cardiomyocyte hypertrophy (E) as measured by staining with wheat germ agglutinin and DAPI (F) and increased angiogenesis in the infarct zone (G). Less cardiomyocyte death was observed in the border zone of CDC-exosome-treated animals compared to control. (H, I) (D-I n=4 hearts per group) *P<0.05, **P<0.01, ***P<0.001. using Student's t test, all scale bars represent 50 µm. Data represented as mean and standard error of the mean.

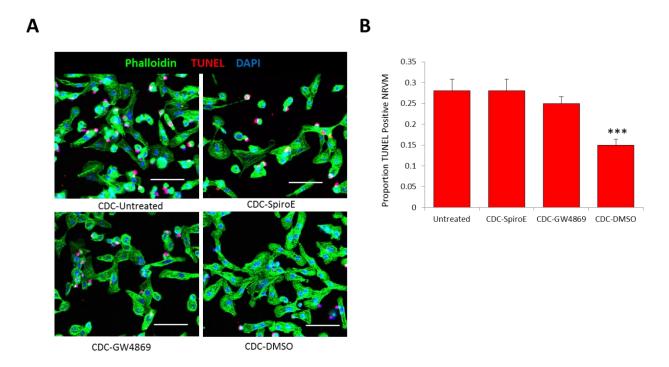
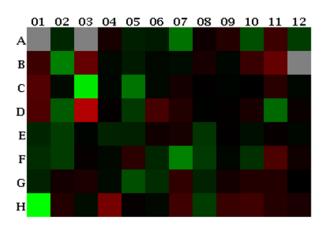
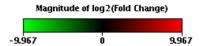


Figure S4. Inhibition of exosome secretion in CDCs diminishes the protective effects of CDCs in vitro, Related to Figure 3

Neonatal rat ventricular myocytes were stressed with 50 μ M H₂O₂ for 15 minutes followed by trans-well treatment with CDCs pre-treated with 5 μ M of Spiroepoxide, 20 μ M of GW4869, or vehicle (DMSO). (A) Cell death was measured using TUNEL staining (red), Phalloidin (green), and DAPI (blue). (B) Pooled data of the four groups represented as proportion of TUNEL positive cardiomyocyte nuclei of total cells counted (n=3 technical replicates from neonatal rat cardiomyocytes derived from 20-30 rat pups from 3 different mothers) (B). *P<0.05, **P<0.01, ***P<0.001 using Student's t test, all scale bars represent 50 μ m. Data represented as mean and standard error of the mean.

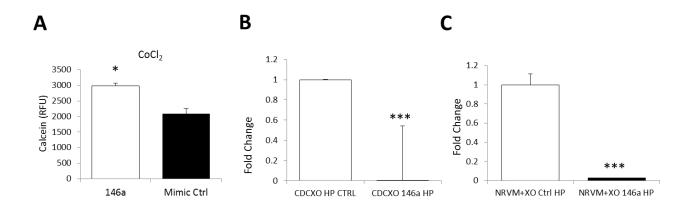




		A03									
A01	A02	hsa-miR-142-	A04	A05	A06	A07	A08	A09	A10	A11	A12
hsa-miR-142-5p	hsa-miR-16	3p	hsa-miR-21	hsa-miR-15a	hsa-miR-29b	hsa-let-7a	hsa-miR-126	hsa-miR-143	hsa-let-7b	hsa-miR-27a	hsa-let-7f
B01	B02	B03	B04	B05	B06	B07	B08	B09	B10	B11	B12
hsa-miR-9	hsa-miR-26a	1	l	hsa-miR-181a	hsa-miR-29a	hsa-miR-124	hsa-miR-144	1	hsa-miR-19b	I	hsa-miR-122
CO1	C02	C03	C04	C05	C06	C07	C08	C09	C10	C11	C12
hsa-miR-150	hsa-miR-32	1	l	ı	l	1	ı	l		hsa-miR-130a	
											D12
D01	D02	D03	D04	D05	D06	D07	D08	D09	D10	D11	hsa-miR-
hsa-miR-27b	hsa-miR-26b	hsa-miR-146a	hsa-miR-200c	hsa-miR-99a	hsa-miR-19a	hsa-miR-23a	hsa-miR-30a	hsa-let-7i	hsa-miR-93	hsa-let-7c	106b
E01	E02	E03	E04	E05	E06	E07	E08	E09	E10	E11	E12
hsa-miR-101	hsa-let-7g	hsa-miR-425	hsa-miR-15b	hsa-miR-28-5p	hsa-miR-18a	hsa-miR-25	hsa-miR-23b	hsa-miR-302a	hsa-miR-186	hsa-miR-29c	hsa-miR-7
	1						F08		F10	F11	
F01	F02	F03	F04	F05	F06	F07	hsa-miR-151-	F09	hsa-miR-	hsa-miR-140-	F12
hsa-let-7d	hsa-miR-30c	hsa-miR-181b	hsa-miR-223	hsa-miR-320a	hsa-miR-374a	hsa-let-7e	5p	hsa-miR-374b	196b	3р	hsa-miR-100
					G06	G07			G10		G12
G01	G02	G03	G04	G05	hsa-miR-423-	hsa-miR-	G08	G09	hsa-miR-28-	G11	hsa-miR-
hsa-miR-103	hsa-miR-96	hsa-miR-302b	hsa-miR-194	hsa-miR-125a-5p	5p	376c	hsa-miR-195	hsa-miR-222	3р	hsa-miR-128	302c
H01	H02	H03	H04	H05							
hsa-miR-423-3p	hsa-miR-185	hsa-miR-30b	hsa-miR-210	SNORD48							

Figure S5. Heat map of MiR PCR array identifies miR-146a as the most differentially expressed miR, Related to Figure 4

Heat map showing fold regulation differential abundance data for transcripts between CDC exosomes and NHDF exosomes overlaid onto the PCR Array plate layout.



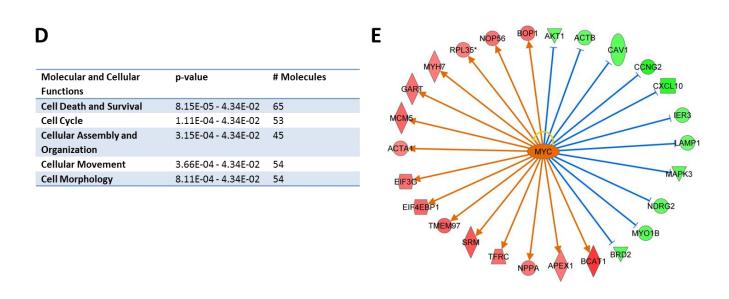


Figure S6. miR-146a protects stressed neonatal rat cardiomyocytes, Related to Figures 4 and 5

(A) Cardiomyocytes were pre-treated with 80 nM miR-146a mimic or mimic-control then exposed to 5 mM cobalt chloride for 2 hours (n=4 technical replicates per group of neonatal rat cardiomyocytes derived from 20-30 rat pups from 3 different mothers) (B, C) CDC exosomes derived from CDCs transfected with mir-146a hairpin inhibitor. Exosomes were derived from conditioned media and mir-146a knockdown confirmed by qPCR in exosomes. (C) Decreased levels of mir-146a in NRVMs treated with 146a-free exosomes compared to control (n=3 technical replicates per group of neonatal rat cardiomyocytes derived from 20-30 rat pups from 3 different mothers). Pathway analysis derived from transcriptome data showing affected pathways and (B) Pathway depiction showing MYC activation as a putative hub, based on microarray data analysis.

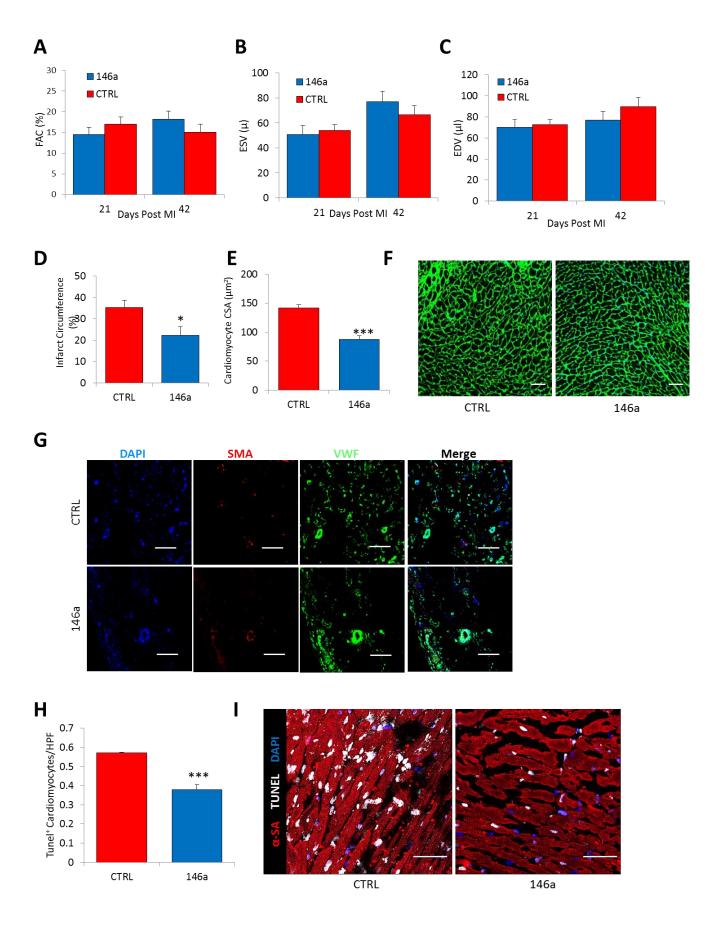


Figure S7. MiR-146a reproduces some but not all the effects of CDC-exosomes, Related to Figure 5

MiR-146a attenuates adverse remodeling and cardiac hypertrophy in a mouse model of chronic MI. (A-C) Animals treated with CDC-exosomes showed no significant functional improvement compared to control as shown by fractional area change (A) , end systolic volume (B) and end diastolic volume (C) (A-C, n=6 animals per group). Structural improvements however were noted as seen in percent of the circumference of tissue sections that are scar (D), and decreased cardiomyocyte hypertrophy (E) as measured by staining with wheat germ agglutinin and DAPI. No differences in angiogenesis were observed between the two groups (G). Less cardiomyocyte death was observed in the border zone of mir 146a-treated animals compared to control. (H, I) (D-I, n=4 hearts per group) *P<0.05, **P<0.01, ***P<0.001 using Student's t test, all scale bars represent 50 μ m. Data represented as mean and standard error of the mean.